

Regulation of mitochondrial gene expression is greatly achieved via degradation pathways where aberrant transcripts, intermediates of transcription or processing are removed. The key player in yeast mitochondria responsible for RNA quality control is the mitochondrial degradosome complex. The complex is composed of two subunits: RNA helicase Suv3p which is highly conserved in all eukaryotes and an exoribonuclease Dss1p whose orthologs are found only in fungi. Because RNA decay is a crucial element in cell metabolism deciphering the structure of the key complex responsible for RNA surveillance in yeast mitochondria would greatly contribute to the description of mechanisms behind this process.

#### Results:

We have tested 30 native crystals of the mitochondrial degradosome complex and 20 selenomethionine derivatives of both subunits of the complex. We hoped to trace the N-terminal part of the Suv3 protein which lacks sequence identity with the human homolog hSuv3p (pdb entry: 3rc8), however the crystals diffracted poorly up to 8 Å. We've collected 5 data sets from native crystals using helical mode for data collection. The best one with the resolution 3.2 Å and 5 standard data sets of around 3.5 Å. The collected data sets were automatically processed in space group P1, C222 or C2221. We were able to solve the structure of the mtEXO complex in C2221 space group by molecular replacement using as a search model the human Suv3 protein and previously solved by SAD the Dss1 protein.